

SEQUENCE LISTING

<110> Boylan, John  
Bowers, Alex

<120> Novel Serine Threonine Kinase Member, h2520-59

<130> 01017/36524A

<150> US 60/219,204

<151> 2000-07-19

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 2059

<212> DNA

<213> Homo sapiens

<220>

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Thr Pro Leu Ala Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu	
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gag ttg gat gac aac tta gat acc gag cgt ccc gtc cag aaa cga gct	153
Glu Leu Asp Asp Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala	
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cga agt ggg ccc cag ccc aga ctg ccc ccc tgc ctg ttg ccc ctg agc	201
Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser	
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Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr Ala Ser Arg	
55 60 65	
ctt ggg ccc tat gtc ctc ctg gag ccc gag gag ggc ggg cgg gcc tac	297
Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly Arg Ala Tyr	
70 75 80	
cgg gcc ctg cac tgc cct aca ggc act gag tat acc tgc aag gtg tac	345
Arg Ala Leu His Cys Pro Thr Gly Thr Glu Tyr Thr Cys Lys Val Tyr	
85 90 95	
ccc gtc cag gaa gcc ctg gcc gtg ctg gag ccc tac gcg cgg ctg ccc	393
Pro Val Gln Glu Ala Leu Ala Val Leu Glu Pro Tyr Ala Arg Leu Pro	
100 105 110 115	

ccg cac aag cat gtg gct cgg ccc act gag gtc ctg gct ggt acc cag Pro His Lys His Val Ala Arg Pro Thr Glu Val Leu Ala Gly Thr Gln 120 125 130	441
ctc ctc tac gcc ttt ttc act cgg acc cat ggg gac atg cac agc ctg Leu Leu Tyr Ala Phe Phe Thr Arg Thr His Gly Asp Met His Ser Leu 135 140 145	489
gtg cga agc cgc cac cgt atc cct gag cct gag gct gcc gtg ctc ttc Val Arg Ser Arg His Arg Ile Pro Glu Pro Glu Ala Ala Val Leu Phe 150 155 160	537
cgc cag atg gcc acc gcc ctg gcg cac tgt cac cag cac ggt ctg gtc Arg Gln Met Ala Thr Ala Leu Ala His Cys His Gln His Gly Leu Val 165 170 175	585
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ctg ggg ctg gac gaa gcc agg gaa gag gag gga gac aga gaa gtg gtt Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg Glu Val Val 340 345 350 355	1113

ctg tat ggc taggaccacc ctactacacg ctacagctgcc aacagtggat 1162  
Leu Tyr Gly

tgagtttggg ggtagctcca agccttctcc tgcctctgaa ctgagccaaa ccttcagtgc 1222  
cttcacagaag ggagaaaaggc agaagcctgt gtggagtgtg ctgtgtacac atctgctttg 1282  
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20 25 30

Lys Arg Ala Arg Ser Gly Pro Gln Pro Arg Leu Pro Pro Cys Leu Leu  
35 40 45

Pro Leu Ser Pro Pro Thr Ala Pro Asp Arg Ala Thr Ala Val Ala Thr  
50 55 60

Ala Ser Arg Leu Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly  
65 70 75 80

Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala Gln Val Val  
325 330 335

Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu Gly Asp Arg  
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Glu Val Val Leu Tyr Gly  
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<212> DNA  
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21

<210> 4  
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21

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Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
1 5 10

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cggggcgaga tgcgagccac

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aggggtgggtcc tagccataca

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Lys	Arg	Leu	Glu	Leu	Asp	Asp	Asn	Leu	Asp	Thr	Glu	Arg	Pro	Val	Gln	
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Lys	Arg	Ala	Arg	Ser	Gly	Pro	Gln	Pro	Arg	Leu	Pro	Pro	Cys	Leu	Leu	
		35					40					45				
Pro	Leu	Ser	Pro	Pro	Thr	Ala	Pro	Asp	Arg	Ala	Thr	Ala	Val	Ala	Thr	
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Ala	Ser	Arg	Leu	Gly	Pro	Tyr	Val	Leu	Leu	Glu	Pro	Glu	Glu	Gly	Gly	
65					70					75					80	
Arg	Ala	Tyr	Gln	Ala	Leu	His	Cys	Pro	Thr	Gly	Thr	Glu	Tyr	Thr	Cys	
				85					90					95		
Lys	Val	Tyr	Pro	Val	Gln	Glu	Ala	Pro	Ala	Val	Leu	Glu	Pro	Tyr	Ala	
			100					105					110			
Arg	Leu	Pro	Pro	His	Lys	His	Val	Ala	Arg	Pro	Thr	Glu	Val	Leu	Ala	
		115					120					125				
Gly	Thr	Gln	Leu	Leu	Tyr	Ala	Phe	Phe	Thr	Arg	Thr	His	Gly	Asp	Met	
		130				135					140					
His	Ser	Leu	Val	Arg	Ser	Arg	His	Arg	Ile	Pro	Glu	Pro	Glu	Ala	Ala	
145					150					155					160	
Val	Leu	Phe	Arg	Gln	Met	Ala	Thr	Ala	Leu	Ala	His	Cys	His	Gln	His	
				165					170					175		
Gly	Leu	Val	Leu	Arg	Asp	Leu	Lys	Leu	Cys	Arg	Phe	Val	Phe	Ala	Asp	
			180					185					190			
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Gln	Gly	Trp 35	Ser	Trp	Ala	Gly	Ile 40	Pro	Ser	Ser	Ala	Ala 45	Ala	Gln	Arg
Ala	Gly 50	Pro	Pro	Ala	Gly	Ala 55	Leu	Glu	Ala	Leu	Ser 60	Pro	Gly	Gly	Ala
Arg 65	Ala	His	Ala	Glu	Arg 70	Arg	Gly	Glu	Met	Arg 75	Ala	Thr	Pro	Leu	Ala 80
Ala	Pro	Ala	Gly	Ser 85	Leu	Ser	Arg	Lys	Lys 90	Arg	Leu	Glu	Leu	Asp 95	Asp
Asn	Leu	Asp	Thr 100	Glu	Arg	Pro	Val	Gln 105	Lys	Arg	Ala	Arg	Ser 110	Gly	Pro
Gln	Pro	Arg 115	Leu	Pro	Pro	Cys	Leu 120	Leu	Pro	Leu	Ser	Pro 125	Pro	Thr	Ala

Pro Asp Arg Ala Thr Ala Val Xaa Thr Xaa Ser Arg Xaa Xaa Xaa Tyr  
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Val Leu Leu Glu Ala Arg Arg Xaa Ala  
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20 25 30

Glu Ala Ala Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys  
35 40 45

His Gln His Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val  
50 55 60

Phe Ala Asp Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp  
65 70 75 80

Ser Cys Val Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala  
85 90 95

Cys Pro Ala Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr  
100 105 110

Ser Gly Lys Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr  
115 120 125

Met Leu Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu  
130 135 140

Phe Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser  
145 150 155 160

Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala  
165 170 175

Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln  
180 185 190

Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala  
195 200 205

Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu  
210 215 220

Gly Asp Arg Glu Val Val Leu Tyr Gly  
225 230

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Ala	Ala 50	Pro	Ala	Gly	Ser	Leu 55	Ser	Arg	Lys	Lys	Arg 60	Leu	Glu	Leu	Asp
Asp 65	Asn	Leu	Asp	Thr	Glu 70	Arg	Pro	Val	Gln	Lys 75	Arg	Ala	Arg	Ser	Gly 80
Pro	Gln	Pro	Arg	Leu 85	Pro	Pro	Cys	Leu 90	Leu	Pro	Leu	Ser	Pro	Pro 95	Thr
Ala	Pro	Asp	Arg 100	Ala	Thr	Ala	Val	Ala 105	Thr	Ala	Ser	Arg	Leu 110	Gly	Pro
Tyr	Val	Leu 115	Leu	Glu	Pro	Glu	Glu 120	Gly	Gly	Arg	Ala 125	Tyr	Gln	Ala	Leu
His	Cys 130	Pro	Thr	Gly	Thr	Glu 135	Tyr	Thr	Cys	Lys	Val 140	Tyr	Pro	Val	Gln
Glu 145	Ala	Leu	Ala	Val	Leu 150	Glu	Pro	Tyr	Ala	Arg 155	Leu	Pro	Pro	His	Lys 160
His	Val	Ala	Arg	Pro 165	Thr	Glu	Val	Leu	Ala 170	Gly	Thr	Gln	Leu	Leu 175	Tyr
Ala	Phe	Phe	Thr 180	Arg	Thr	His	Gly	Asp 185	Met	His	Ser	Leu	Val 190	Arg	Ser
Arg	His	Arg 195	Ile	Pro	Glu	Pro	Glu 200	Ala	Ala	Val	Leu	Phe 205	Arg	Gln	Met
Ala	Thr 210	Ala	Leu	Ala	His	Cys 215	His	Gln	His	Gly	Leu 220	Val	Leu	Arg	Asp
Leu 225	Lys	Leu	Cys	Arg	Phe 230	Val	Phe	Ala	Asp	Arg 235	Glu	Arg	Lys	Lys	Leu 240
Val	Leu	Glu	Asn	Leu 245	Glu	Asp	Ser	Cys	Val 250	Leu	Thr	Gly	Pro	Asp 255	Asp
Ser	Leu	Trp	Asp 260	Lys	His	Ala	Cys	Pro 265	Ala	Tyr	Val	Gly	Pro 270	Glu	Ile
Leu	Ser	Ser 275	Arg	Ala	Ser	Tyr	Ser 280	Gly	Lys	Ala	Ala	Asp 285	Val	Trp	Ser
Leu	Gly 290	Val	Ala	Leu	Phe	Thr 295	Met	Leu	Ala	Gly	His 300	Tyr	Pro	Phe	Gln

Asp Ser Glu Pro Val Leu Leu Phe Gly Lys Ile Arg Arg Gly Ala Tyr  
 305 310 315 320  
 Ala Leu Pro Ala Gly Leu Ser Ala Pro Ala Arg Cys Leu Val Arg Cys  
 325 330 335  
 Leu Leu Arg Arg Glu Pro Ala Glu Arg Leu Thr Ala Thr Gly Ile Leu  
 340 345 350  
 Leu His Pro Trp Leu Arg Gln Asp  
 355 360

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 gacctgagat actcagctca cgggcctcat actcgggcaa ggcagccgat gtctggagcc 180  
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 ctgcccgtg tctggttcgc tgccctcttc gtcgggagcc agctgaacgg ctcacagcca 360  
 caggcatcct cctgcacccc tggctgcgac aggaccgat gcccttagcc ccaaccgat 420  
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 aagaggaggg agacagagaa gtggttctgt 510

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 Arg Ser Gly Pro Gln Pro Arg Leu Cys  
 20 25

<210> 14  
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<400> 14

Gly Pro Tyr Val Leu Leu Glu Pro Glu Glu Gly Gly Arg Ala Tyr Gln  
 1 5 10 15

<400> 15

Leu Asp Glu Ala Arg Glu Glu Glu Cys  
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